

9/12 #8



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RAW SEQUENCE LISTING

DATE: 09/17/2002

PATENT APPLICATION: US/10/005,228

TIME: 13:30:41

Input Set : A:\Gi-554.app

Output Set: N:\CRF4\09172002\J005228.raw

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3 <110> APPLICANT: Lyons, Karen M
5 <120> TITLE OF INVENTION: Method and Composition for Modulating Bone Growth
7 <130> FILE REFERENCE: 22058-554
9 <140> CURRENT APPLICATION NUMBER: 10/005,228
10 <141> CURRENT FILING DATE: 2001-12-03
12 <150> PRIOR APPLICATION NUMBER: 60/250,535
13 <151> PRIOR FILING DATE: 2000-12-01
15 <160> NUMBER OF SEQ ID NOS: 9
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2952
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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27 ccttcccccc tcgccctcat gaatagctgg gactacagcc tggagcattg gtaagcgtca 180
28 cactgccaaa gtgagagctg ctggagaact cataatccca ggaacgcctc ttctactctc 240
29 cgagtacccc agtgaccaga gtgagagaag ctctgaacga gggcacgcgg cttgaaggac 300
30 tgtgggcaga tgtgaccaag agcctgcatt aagttgtaca atggtagatg gagtgatgat 360
31 tcttctctgt cttatcatga ttgctctccc ctcccctagt atggaagatg agaagcccaa 420
32 ggtcaacccc aaactctaca tgtgtgtgtg tgaaggtctc tcctgcggta atgaggacca 480
33 ctgtgaaggc cagcagtgc tttcctcact gagcatcaac gatggcctcc acgtctacca 540
34 gaaaggctgc ttccaggttt atgagcaggg aaagatgacc tgtaagaccc cgccgtcccc 600
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36 gccactaaa ggaaaatcct tccttggaa acagaatttc cacttggagg ttggcctcat 720
37 tattctctct gtagtgttcg cagtatgtct tttagcctgc ctgctgggag ttgctctccg 780
38 aaaatttaaa aggcgcaacc aagaacgcct caatccccga gacgtggagt atggcactat 840
39 cgaagggtct atcaccacca atgttgagga cagcacttta gcagatttat tggatcattc 900
40 gtgtacatca ggaagtggct ctggtcttcc ttttctggta caaagaacag tggctcgcca 960
41 gattacactg ttggagtgtg tcgggaaagg caggtatggt gaggtgtgga ggggcagctg 1020
42 gcaaggggaa aatgttgccg tgaagatctt ctccctccgt gatgagaagt catggttcag 1080
43 ggaaacggaa ttgtacaaca ctgtgatgct gaggcataaa aatatcttag gtttcattgc 1140
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51 tggacttggt ttgtgggaag tggccaggcg gatggtgagc aatggtatag tggaggatta 1620
52 caagccaccg ttctacgat tggttcccaa tgacccaagt tttgaagata tgaggaaggt 1680
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54 aacctctctg gccaaagctaa tgaagaatg ctggtatcaa aatccatccg caagactcac 1800
55 agcactgcgt atcaaaaaga ctttgaccaa aattgataat tccctcgaca aattgaaaac 1860
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57 ctgggaccta atgctggcct gactggttgt cagaatggaa tccatctgtc tccctcccca 1980
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60 gactaatgtt ggacagacac tgttgcaaag gtagggactg gaggaacaca gagaaatcct 2160
61 aaaagagatc tgggcattaa gtcagtggct ttgcatagct ttcacaagtc tcctagacac 2220
62 tccccacggg aaactcaagg aggtggtgaa tttttaatca gcaatattgc ctgtgcttct 2280
63 cttctttatt gcaactaggaa ttctttgcat tccttacttg cactgttact cttaatttta 2340
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70 gtaacttttt ttcatgtcat atgcagaacg tatttagcca ttaccacgt gacaccaccg 2760
71 aatatattat cgatttagaa gcaaagattt cagtagaatt ttagtctga acgctacggg 2820
72 gaaatgcat tttcttcaga attatccatt acgtgcattt aaactctgcc agaaaaaaat 2880
73 aactattttg ttttaatcta ctttttgtat ttagtagtta tttgtataaa ttaaataaac 2940
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77 <210> SEQ ID NO: 2

78 <211> LENGTH: 509

79 <212> TYPE: PRT

80 <213> ORGANISM: Homo sapiens

82 <400> SEQUENCE: 2

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84 1 5 10 15
86 Pro Ser Pro Ser Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu
87 20 25 30
89 Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys
90 35 40 45
92 Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His
93 50 55 60
95 Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr
96 65 70 75 80
98 Cys Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly
99 85 90 95
101 Asp Trp Cys Asn Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys
102 100 105 110
104 Ser Phe Pro Gly Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile
105 115 120 125
107 Leu Ser Val Val Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val
108 130 135 140
110 Ala Leu Arg Lys Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg
111 145 150 155 160
113 Asp Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly
114 165 170 175
116 Asp Ser Thr Leu Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser

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117          180          185          190
119 Gly Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile
120          195          200          205
122 Thr Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg
123          210          215          220
125 Gly Ser Trp Gln Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg
126 225          230          235          240
128 Asp Glu Lys Ser Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met
129          245          250          255
131 Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser
132          260          265          270
134 Arg His Ser Ser Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met
135          275          280          285
137 Gly Ser Leu Tyr Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser
138          290          295          300
140 Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His
141 305          310          315          320
143 Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp
144          325          330          335
146 Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile
147          340          345          350
149 Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu
150          355          360          365
152 Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro
153          370          375          380
155 Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys
156 385          390          395          400
158 Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg
159          405          410          415
161 Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr
162          420          425          430
164 Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val
165          435          440          445
167 Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp
168          450          455          460
170 Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln
171 465          470          475          480
173 Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr
174          485          490          495
176 Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys
177          500          505
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181 <211> LENGTH: 1969
182 <212> TYPE: DNA
183 <213> ORGANISM: Homo sapiens
185 <400> SEQUENCE: 3
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188 gagegagccc ctccccggct ccagcccggg ccggggccgc gccggacccc agcccgcgcg 180

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190 aggctagcgc cccgccaccc gcagagcggg cccagaggga ccatgacctt gggctcccc 300
191 aggaaaggcc ttctgatgct gctgatggcc ttggtgacct agggagacct tgtgaagccg 360
192 tctcggggcc cgctggtgac ctgcacgtgt gagagccac attgcaagg gcctacctgc 420
193 cggggggcct ggtgcacagt agtgctggtg cgggaggagg ggaggcaccc ccaggaacat 480
194 cggggctgcg ggaacttgca caggagactc tgcagggggc gccccaccga gttcgtcaac 540
195 cactactgct gcgacagcca cctctgcaac cacaacgtgt ccctggtgct ggaggccacc 600
196 caacctcctt cggagcagcc ggaacagat ggccagctgg ccctgatcct gggccccgtg 660
197 ctggccttgc tggccctggt ggccttgggt gtccctgggc tgtggcatgt ccgacggagg 720
198 caggagaagc agcgtggcct gcacagcgag ctgggagagt ccagtctcat cctgaaagca 780
199 tctgagcagg gcgacacgat gttgggggac ctctggaca gtgactgcac cacagggagt 840
200 ggctcagggc tcccccttct ggtgcagagg acagtggcac ggcaggttgc cttggtggag 900
201 tgtgtgggaa aaggccgcta tggcgaagtg tggcggggct tgtggcacgg tgagagtgtg 960
202 gccgtcaaga tcttctctc gagggatgaa cagtcctggt tccgggagac tgagatctat 1020
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204 cgcaactcga gcacgcagct gtggtctatc acgcactacc acgagcacgg ctccctctac 1140
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209 acccgagagt gggcaccaag cgttacatgg caccgaggt gctggacgag cagatccgca 1440
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211 agattgcccg ccggaccatc gtgaatggca tcgtggagga ctatagacca cccttctatg 1560
212 atgtggtgcc caatgacccc agctttgagg acatgaagaa ggtggtgtgt gtggatcagc 1620
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215 agacactaca aaaaattagc aacagtccag agaagcctaa agtgattcaa tagcccagga 1800
216 gcacctgatt cttttctgcc tgcagggggc tgggggggtg gggggcagtg gatggtgcc 1860
217 tatctgggta gaggtagtgt gagtgtggtg tgtgctgggg atgggcagct gcgcctgcct 1920
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221 <210> SEQ ID NO: 4

222 <211> LENGTH: 503

223 <212> TYPE: PRT

224 <213> ORGANISM: Homo sapiens

226 <400> SEQUENCE: 4

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231           20           25           30
233 Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
234           35           40           45
236 Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
237           50           55           60
239 Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
240           65           70           75           80
242 Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
243           85           90           95
245 His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
246           100          105          110

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248 Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala
249      115      120      125
251 Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
252      130      135      140
254 Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
255 145      150      155      160
257 Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp
258      165      170      175
260 Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
261      180      185      190
263 Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
264      195      200      205
266 Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
267      210      215      220
269 Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
270 225      230      235      240
272 Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile
273      245      250      255
275 Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
276      260      265      270
278 Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
279      275      280      285
281 Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
282      290      295      300
284 Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
285 305      310      315      320
287 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
288      325      330      335
290 Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
291      340      345      350
293 Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
294      355      360      365
296 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
297      370      375      380
299 Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
300 385      390      395      400
302 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
303      405      410      415
305 Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
306      420      425      430
308 Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
309      435      440      445
311 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
312      450      455      460
314 Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
315 465      470      475      480
317 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
318      485      490      495
320 Glu Lys Pro Lys Val Ile Gln

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VERIFICATION SUMMARY

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